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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/422,548*

DATE: 07/11/95
TIME: 09:23:37

INPUT SET: S4668

TEAM 6

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

```
1                                SEQUENCE LISTING
2
3   (1)    General Information:
4
5    (i) APPLICANT: Eaton, Dan L.
6                   DeSauvage, Frederic J.
7
8   (ii) TITLE OF INVENTION: MPL LIGAND
9
10  (iii) NUMBER OF SEQUENCES: 32
11
12   (iv) CORRESPONDENCE ADDRESS:
13        (A) ADDRESSEE: Genentech, Inc.
14        (B) STREET: 460 Point San Bruno Blvd
15        (C) CITY: South San Francisco
16        (D) STATE: California
17        (E) COUNTRY: USA
18        (F) ZIP: 94080
19
20    (v) COMPUTER READABLE FORM:
21        (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
22        (B) COMPUTER: IBM PC compatible
23        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24        (D) SOFTWARE: patin (Genentech)
25
26   (vi) CURRENT APPLICATION DATA:
27        (A) APPLICATION NUMBER:
28        (B) FILING DATE: 13-APR-1995
29        (C) CLASSIFICATION:
30
31  (vii) PRIOR APPLICATION DATA:
32        (A) APPLICATION NUMBER: 08/223263
33        (B) FILING DATE: 04-APR-1994
34
35  (vii) PRIOR APPLICATION DATA:
36        (A) APPLICATION NUMBER: 08/196689
37        (B) FILING DATE: 15-FEB-1994
38
39  (vii) PRIOR APPLICATION DATA:
40        (A) APPLICATION NUMBER: 08/185607
41        (B) FILING DATE: 21-JAN-1994
42
43  (vii) PRIOR APPLICATION DATA:
44        (A) APPLICATION NUMBER: 08/176553
45        (B) FILING DATE: 03-JAN-1994
46
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47   (viii) ATTORNEY/AGENT INFORMATION:
48          (A) NAME: Winter, Daryl B.
49          (B) REGISTRATION NUMBER: 32,637
50          (C) REFERENCE/DOCKET NUMBER: 871P3D1
51
52    (ix) TELECOMMUNICATION INFORMATION:
53          (A) TELEPHONE: 415/225-1249
54          (B) TELEFAX: 415/952-9881
55          (C) TELEX: 910/371-7168
56
57   (2) INFORMATION FOR SEQ ID NO:1:
58
59     (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 353 amino acids
61          (B) TYPE: amino acid
62          (D) TOPOLOGY: linear
63
64    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66   Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
67     1               5                  10                  15
68
69   Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
70                    20                  25                  30
71
72   Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
73                    35                  40                  45
74
75   Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
76                    50                  55                  60
77
78   Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
79                    65                  70                  75
80
81   Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
82                    80                  85                  90
83
84   Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
85                    95                 100                 105
86
87   Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
88                   110                 115                 120
89
90   Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
91                   125                 130                 135
92
93   Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
94                   140                 145                 150
95
96   Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
97                   155                 160                 165
98
99   Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
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100                         170                   175                   180
101
102     Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
103                         185                   190                   195
104
105     Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
106                         200                   205                   210
107
108     Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
109                         215                   220                   225
110
111     Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
112                         230                   235                   240
113
114     Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
115                         245                   250                   255
116
117     Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
118                         260                   265                   270
119
120     Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
121                         275                   280                   285
122
123     Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
124                         290                   295                   300
125
126     Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
127                         305                   310                   315
128
129     Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
130                         320                   325                   330
131
132     Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
133                         335                   340                   345
134
135     Ser Gln Asn Leu Ser Gln Glu Gly
136                         350           353
137
138     (2) INFORMATION FOR SEQ ID NO:2:
139
140        (i) SEQUENCE CHARACTERISTICS:
141            (A) LENGTH: 1795 bases
142            (B) TYPE: nucleic acid
143            (C) STRANDEDNESS: single
144            (D) TOPOLOGY: linear
145
146       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
147
148
149     TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
150
151
152     CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
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153
154
155   CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
156
157
158   CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
159
160
161   GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
162
163
164   TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
165
166
167   ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
168
169
170   AGACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
171
172
173   GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
174
175
176   CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
177
178
179   ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
180
181
182   GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
183
184
185   TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
186
187
188   AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
189
190
191   CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750
192
193
194   CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
195
196
197   CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
198
199
200   AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
201
202
203   TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
204
205
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INPUT SET: S4668.raw

```
206    TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC 1000
207
208
209    TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050
210
211
212    CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100
213
214
215    CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150
216
217
218    CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200
219
220
221    CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
222
223
224    TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
225
226
227    AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350
228
229
230    AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
231
232
233    GGGATACACA GGACTGAAAA GGGAATCATT TTTCACTGTA CATTATAAAC 1450
234
235
236    CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
237
238
239    GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550
240
241
242    TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
243
244
245    GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
246
247
248    TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700
249
250
251    CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750
252
253
254    AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAA AAAAA 1795
255
256
257
258    (2) INFORMATION FOR SEQ ID NO:3:
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/422,548*

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Line   Error   Original Text